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SUPERIOR COURT OF WASHINGTON FOR KING COUNTY

STATE OF WASHINGTON,

Plaintiff,

vs.

EMANUEL FAIR,

Defendant.

No. 10-1-09274-5 SEA

DECLARATION OF JOANNE B. SGUEGLIA

I, Joanne B. Sgueglia, hereby declare as follows:

1. I am over 18 years of age and I am competent to make this declaration.
2. I hold the following academic degrees: BA with Honors, SUNY Purchase
3. I am currently employed as Sr. Manager, HID Professional Services at Thermo Fisher Scientific
4. I am familiar with Cybergenetics, and its TrueAllele software. TrueAllele is a probabilistic genotyping computer system that interprets DNA evidence using a statistical model. I am familiar with the many TrueAllele validation studies that have established the reliability of the method and software.

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5. In my previous employment at the Massachusetts State Police Crime Laboratory we had validated the TrueAllele case working system (completed in 2011).
6. We have never requested the source code for the TrueAllele software. I do not believe the source code is necessary for determining the reliability of TrueAllele as an applied user and forensic scientist.
7. I have been involved in manual mixture interpretation methods for STR DNA evidence for over 20 years. I have conducted many mixture interpretation workshops and trainings both individually and as part of a joint effort. DNA mixture interpretation training, as it applies to forensic evidence, was conducted internally for all forensic DNA analysts and as part of 6 DNA Academies held at the MA SP laboratory (1999 – 2011), partially in conjunction with the Northeast Regional Forensic Institute (NERFI)/SUNY Albany. Additional external training was provided at national and regional meetings such as the American Academy of Forensic Sciences (AAFS), BODE East, Northeastern Association of Forensic Scientists (NEAFS) and the Green Mountain DNA Conference in Vermont.
8. Since my employ with Thermo Fisher Scientific (formerly Applied Biosystems/Life Technologies) I have conducted teachbacks for validations of STR systems, including mixture studies, in 23 laboratories throughout the US and at several Life Technologies road shows. Specific and customized mixture interpretation training was conducted for the State of Michigan in 2013.
9. I have been involved in forensic DNA research and development/validation efforts for 28 years, spanning many methods and technology advances over the decades. My introduction to True Allele began in 2007 for Database applications as an Expert System. At MA SP we conducted the NDIS developmental validation for the platform for

1 known/convicted offender samples that was approved by the FBI. I gained competence
2 in the case working platform as a certified user in 2010 as part of the validation initiative.

3 10. We compared hundreds of evidentiary profiles in dozens of cases with both manual and
4 True Allele (TA) methods. We were able to make comparative analyses and show
5 absolute concordance for samples with ample DNA and learn the benefits and advantages
6 of using TA for 2 person mixtures with close ratios (1:1) and for disparate ratios (with
7 minor contributors down to approximately 1:20 or 5%). We also ran complex mixtures
8 with more than 2 individuals and found TA to be useful for low level template DNA
9 samples as minor components in these mixtures.

10 11. We put the TA system through rigorous testing and did not find any need to know the
11 source code. We tested many types of mixtures, both known and unknown, and were
12 satisfied with the results. It took many months of testing to gain a level of familiarity
13 and confidence in the system. We were able to understand what evidence was input and
14 got accustomed to the expected output. As data became more uncertain (low level
15 template DNA and stochastic effects) the resulting LR decreased accordingly. Real and
16 mock casework scenarios, along with contrived mixtures, all gave expected results.

17 12. I do not think knowledge of the source code was needed as an end user because the data
18 input was supported by the output. Validation of the system for forensic applications can
19 be accomplished by knowledgeable and experienced forensic scientists who are not
20 necessarily mathematicians or statisticians. Source code review would not normally fall
21 under the area of expertise held by most forensic scientists and would likely not be fully
22 understood and would confound many. It would take years of additional education and
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Daniel T. Satterberg, Prosecuting Attorney
W554 King County Courthouse
516 Third Avenue

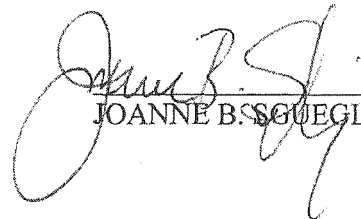
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training to appropriately have the foundation to appropriately review the source code and falls outside the purview of forensic DNA analysts.

13. In the field of forensics, we evaluate and validate many systems by testing our sample types for our applications without specific expertise in the underlying mechanisms, programming, algorithms, chemistry, etc. (e.g. automation and robotics, sizing software, PCR reagents/primer sequences, capillary electrophoresis/polymer composition).

Under penalty of perjury under the laws of the State of Washington, I certify that the foregoing is true and correct to the best of my knowledge and belief.

Signed and dated by me this ___1st___ day of April, 2016, at Carolina Beach, North Carolina.



JOANNE B. SCIEGLIA